

## SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS RELATING TO THE  
 PHARMACOGENETICS OF DIFFERENT GENE VARIANTS

<130> ARCD:405WO

<140> UNKNOWN

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<160> 11

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<210> 1

<211> 4868

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (38)..(4675)

<400> 1

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Arg Ile Val Asn Arg Phe Ala Gly Asp Ile Ser Thr Val Asp Asp Thr	1080	1085	1090	
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Leu Pro Gln Ser Leu Arg Ser Trp Ile Thr Cys Phe Leu Gly Ile Ile	1095	1100	1105	1110
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Thr Lys Phe
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&lt;210&gt; 2

&lt;211&gt; 1545

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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 Leu His Val Tyr Lys Ser Arg Thr Lys Arg Ser Ser Thr Thr Lys Leu  
 50 55 60  
 Tyr Leu Ala Lys Gln Val Phe Val Gly Phe Leu Leu Ile Leu Ala Ala  
 65 70 75 80  
 Ile Glu Leu Ala Leu Val Leu Thr Glu Asp Ser Gly Gln Ala Thr Val  
 85 90 95  
 Pro Ala Val Arg Tyr Thr Asn Pro Ser Leu Tyr Leu Gly Thr Trp Leu  
 100 105 110  
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 Tyr Lys Lys Ala Leu Thr Leu Ser Asn Leu Ala Arg Lys Glu Tyr Thr  
 405 410 415  
 Val Gly Glu Thr Val Asn Leu Met Ser Val Asp Ala Gln Lys Leu Met  
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His	Thr	Gly	Pro	Glu	Glu	Glu	Ala	Thr	Val	His	Asp	Gly	Ser	Glu	Glu	
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 Asp Thr Thr Pro Thr Gly Arg Ile Val Asn Arg Phe Ala Gly Asp Ile  
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 Thr Gln Thr Leu Asn Trp Leu Val Arg Met Thr Ser Glu Ile Glu Thr  
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 Met Asn Leu Asp Pro Phe Asn Asn Tyr Ser Asp Glu Glu Ile Trp Lys  
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 Gly Leu Ser His Glu Val Thr Glu Ala Gly Gly Asn Leu Ser Ile Gly  
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 ttttatgcaa caggaagcat aataggagat ataagacaag cacattgtaa ccttagtaga 180  
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 tctatatttc aatc atg gac caa aat caa cat ttg aat aaa aca gca gag 170  
 Met Asp Gln Asn Gln His Leu Asn Lys Thr Ala Glu  
 1 5 10  
 gca caa cct tca gag aat aag aaa aca aga tac tgc aat gga ttg aag 218  
 Ala Gln Pro Ser Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys  
 15 20 25  
 atg ttc ttg gca gct ctg tca ctc agc ttt att gct aag aca cta ggt 266  
 Met Phe Leu Ala Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly  
 30 35 40  
 gca att att atg aaa agt tcc atc att cat ata gaa cgg aga ttt gag 314

Ala	Ile	Ile	Met	Lys	Ser	Ser	Ile	Ile	His	Ile	Glu	Arg	Arg	Phe	Glu		
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ata	tcc	tct	tct	ctt	gtt	ggt	ttt	att	gac	gga	agc	ttt	gaa	att	gga		362
Ile	Ser	Ser	Ser	Leu	Val	Gly	Phe	Ile	Asp	Gly	Ser	Phe	Glu	Ile	Gly		
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aat	ttg	ctt	gtg	att	gta	ttt	gtg	agt	tac	ttt	gga	tcc	aaa	cta	cat		410
Asn	Leu	Leu	Val	Ile	Val	Phe	Val	Ser	Tyr	Phe	Gly	Ser	Lys	Leu	His		
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aga	cca	aag	tta	att	gga	atc	ggt	tgt	ttc	att	atg	gga	att	gga	ggt		458
Arg	Pro	Lys	Leu	Ile	Gly	Ile	Gly	Cys	Phe	Ile	Met	Gly	Ile	Gly	Gly		
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gtt	ttg	act	gct	ttg	cca	cat	ttc	ttc	atg	gga	tat	tac	agg	tat	tct		506
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Lys	Glu	Thr	Asn	Ile	Asp	Ser	Ser	Glu	Asn	Ser	Thr	Ser	Thr	Leu	Ser		
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Thr	Cys	Leu	Ile	Asn	Gln	Ile	Leu	Ser	Leu	Asn	Arg	Ala	Ser	Pro	Glu		
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Ile	Val	Gly	Lys	Gly	Cys	Leu	Lys	Glu	Ser	Gly	Ser	Tyr	Met	Trp	Ile		
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Tyr	Val	Phe	Met	Gly	Asn	Met	Leu	Arg	Gly	Ile	Gly	Glu	Thr	Pro	Ile		
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gta	cca	ttg	ggg	ctt	tct	tac	att	gat	gat	ttc	gct	aaa	gaa	gga	cat		746
Val	Pro	Leu	Gly	Leu	Ser	Tyr	Ile	Asp	Asp	Phe	Ala	Lys	Glu	Gly	His		
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tct	tct	ttg	tat	tta	ggt	ata	ttg	aat	gca	ata	gca	atg	att	ggt	cca		794
Ser	Ser	Leu	Tyr	Leu	Gly	Ile	Leu	Asn	Ala	Ile	Ala	Met	Ile	Gly	Pro		
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Arg	Trp	Val	Gly	Ala	Trp	Trp	Leu	Asn	Phe	Leu	Val	Ser	Gly	Leu	Phe		
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Ser	Ile	Ile	Ser	Ser	Ile	Pro	Phe	Phe	Phe	Leu	Pro	Gln	Thr	Pro	Asn		
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Lys	Pro	Gln	Lys	Glu	Arg	Lys	Ala	Ser	Leu	Ser	Leu	His	Val	Leu	Glu		
285					290					295					300		

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Asn Ile Thr Lys Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile	
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Val Ser Ser Tyr Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu	
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Leu Cys Glu Asn Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly	
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Ser Asp Cys Asn Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn	
465 470 475	
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Asn Gly Ile Thr Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser	
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Ser Gly Asn Lys Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu	
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